

SEQUENCE LISTING

<110> Rosson, Reinhardt D.
Deng, Ming-de
Grund, Alan D.

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<140> Not Yet Assigned
<141> 2000-04-28

<150> 60/141,798
<151> 1999-06-30

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<170> PatentIn Ver. 2.1

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Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Leu

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25

30

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80

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90

95

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105

110

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115

120

125

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135

140

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Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
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<213> Lactobacillus reuteri

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<223> Xaa = any amino acid

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Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
35 40 45

Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
50 55 60

Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
65 70 75 80

Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
85 90 95

Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
100 105 110

Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
115 120 125

Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
130 135 140

Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys
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Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu
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Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp
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His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His
195 200 205

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210 215 220

Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His
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 245 250 255

Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala
 260 265 270

Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val
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<213> Lactobacillus reuteri

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<213> Lactobacillus reuteri

<220>

<221> CDS

<222> (1)..(1776)

<400> 17

atg tat tat tca aac ggg aat tat gaa gcc ttt gct cga cca aag aag 48
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
1 5 10 15

cct gct ggc gtt gat aag aaa cat gcc tac att gtc ggt ggt ggt tta 96
Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Leu
20 25 30

gct ggt tta tcg gcc gcc gtg ttt tta att cgt gat gcc caa atg ccg 144
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
35 40 45

ggt gag aat atc cat att tta gag gaa tta ccg gtt gcc ggt ggt tct 192
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
50 55 60

ctt gat ggt gaa gat cgt cct gga att ggt ttt gtt act cgt gga ggc 240
Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
65 70 75 80

cgg gaa atg gag aac cat ttc gag tgt atg tgg gac atg tat cgt tca 288
Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
85 90 95

att cca tca ctt gaa atc cca ggt gct tcc tac ctt gat gaa tac tac 336
Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
100 105 110

tgg tta gat aag gaa gat cca aac agt tct aat tgt cgt tta acc tat 384
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
115 120 125

aag cgg gga aat gaa gtt cca tcg gac ggt aaa tat ggt tta agt aaa 432
Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
130 135 140

aag gca atc aaa gag ctg act aag cta att atg acc cct gaa gaa aaa 480
Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys
145 150 155 160

ttg gga agg gag act att ggt gaa tac ttc tct gat gat ttc ttt gaa 528
Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu
165 170 175

agc aat ttc tgg att tat tgg tca aca atg ttt gcg ttt gaa cgg tgg 576
Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp
180 185 190

cac tct cta gct gaa atg cgt cgt tat atg atg cgg ttt att cac cat 624
His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His
195 200 205

att gat ggt tta ccg gat ttc act gca ctg aag ttt aat aag tat aac 672

Ile Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn			
210	215	220	
caa tat gaa tca atg acc aag ccg cta ttg gcc tac ctg aaa gat cat			720
Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His			
225	230	235	240
cat gtc aag att gag tac gat acc cag gta aag aat gtt att gtt gat			768
His Val Lys Ile Glu Tyr Asp Thr Gln Val Lys Asn Val Ile Val Asp			
245	250	255	
act cat ggg cgaa aag cac gct aag cga atc tta tta act caa gcc			816
Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala			
260	265	270	
ggt aaa gat aaa gtt gtt gag tta acg gac aat gac ctt gtc ttt gtc			864
Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val			
275	280	285	
aca aac ggt tca att aca gaa agt tct act tac ggc agt cac cat caa			912
Thr Asn Gly Ser Ile Thr Glu Ser Ser Thr Tyr Gly Ser His His Gln			
290	295	300	
gca gct cga cca acg caa gca ctt ggt ggt agt tgg aaa ctg tgg gaa			960
Ala Ala Arg Pro Thr Gln Ala Leu Gly Gly Ser Trp Lys Leu Trp Glu			
305	310	315	320
aac ctt gct cgg cag tca gct gat ttt ggt cat cct gat gtc ttt tgc			1008
Asn Leu Ala Arg Gln Ser Ala Asp Phe Gly His Pro Asp Val Phe Cys			
325	330	335	
aag aat ctt cca ggg aga agc tgg ttc att tcc gct act gca acc gtt			1056
Lys Asn Leu Pro Gly Arg Ser Trp Phe Ile Ser Ala Thr Ala Thr Val			
340	345	350	
aag aac ccg caa gtt gaa cca tac att gaa cgc tta acc aag cga gat			1104
Lys Asn Pro Gln Val Glu Pro Tyr Ile Glu Arg Leu Thr Lys Arg Asp			
355	360	365	
ctc cat gat ggc aaa gtt aat act ggt gga atc att acg gtc act gac			1152
Leu His Asp Gly Lys Val Asn Thr Gly Gly Ile Ile Thr Val Thr Asp			
370	375	380	
tct aat tgg atg ctt tcc tgg aca att cac cgt caa ccg cac ttc aag			1200
Ser Asn Trp Met Leu Ser Trp Thr Ile His Arg Gln Pro His Phe Lys			
385	390	395	400
aaa caa aag aaa aat gaa acc att gtt tgg att tac ggt ctg tac tct			1248
Lys Gln Lys Lys Asn Glu Thr Ile Val Trp Ile Tyr Gly Leu Tyr Ser			
405	410	415	
aat aca aag gga aac tat att aag aaa ccg atc gtt gat tgt act ggt			1296
Asn Thr Lys Gly Asn Tyr Ile Lys Lys Arg Ile Val Asp Cys Thr Gly			
420	425	430	
gaa gag att act aaa gaa tgg cta tcc atc tgg ggg ttc cag aag ccg			1344
Glu Glu Ile Thr Lys Glu Trp Leu Ser Ile Trp Gly Phe Gln Lys Pro			
435	440	445	
tta att gac gat ttg gct aag gag agt tca att aat act gtt cca gta			1392
Leu Ile Asp Asp Leu Ala Lys Glu Ser Ser Ile Asn Thr Val Pro Val			

450

455

460

tat atg cca ttt atc act agc tac ttt atg cca cga gtt aag ggc gac Tyr Met Pro Phe Ile Thr Ser Tyr Phe Met Pro Arg Val Lys Gly Asp 465 470 475 480	1440
cgt cca gac gtt gtt cca gaa gga tcc gct aac ttg gca ttt att ggt Arg Pro Asp Val Val Pro Glu Gly Ser Ala Asn Leu Ala Phe Ile Gly 485 490 495	1488
aac ttt gct gaa tct cca agt cga gat acc gta ttt acc acg gaa tat Asn Phe Ala Glu Ser Pro Ser Arg Asp Thr Val Phe Thr Thr Glu Tyr 500 505 510	1536
tca gta cg ^g acc gca atg gaa gcc gtc tac act cta tta gat gtt gat Ser Val Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asp Val Asp 515 520 525	1584
cg ^g gga gtt cca gaa gtc ttt aac tct att tat gat ctt cga gag tta Arg Gly Val Pro Glu Val Phe Asn Ser Ile Tyr Asp Leu Arg Glu Leu 530 535 540	1632
atg cg ^g gca atg tat tac atg aat gat aag aag cc ^g tta aaa gac atg Met Arg Ala Met Tyr Tyr Met Asn Asp Lys Lys Pro Leu Lys Asp Met 545 550 555 560	1680
gac ttg cca att cca aag att gtt gaa aag cca tta tta aag aaa ctc Asp Leu Pro Ile Pro Lys Ile Val Glu Lys Pro Leu Leu Lys Lys Leu 565 570 575	1728
caa gga acg tgg att ggt gaa tta atg gag caa cag cac tta cta taa Gln Gly Thr Trp Ile Gly Glu Leu Met Glu Gln Gln His Leu Leu 580 585 590	1776

<210> 18

<211> 591

<212> PRT

<213> Lactobacillus reuteri

<400> 18

Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys 1 5 10 15
Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Leu 20 25 30
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro 35 40 45
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser 50 55 60
Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly 65 70 75 80
Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser 85 90 95
Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr 100 105 110
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr 115 120 125
Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys 130 135 140
Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys 145 150 155 160

Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu
 165 170 175
 Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp
 180 185 190
 His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His
 195 200 205
 Ile Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn
 210 215 220
 Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His
 225 230 235 240
 His Val Lys Ile Glu Tyr Asp Thr Gln Val Lys Asn Val Ile Val Asp
 245 250 255
 Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala
 260 265 270
 Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val
 275 280 285
 Thr Asn Gly Ser Ile Thr Glu Ser Ser Thr Tyr Gly Ser His His Gln
 290 295 300
 Ala Ala Arg Pro Thr Gln Ala Leu Gly Gly Ser Trp Lys Leu Trp Glu
 305 310 315 320
 Asn Leu Ala Arg Gln Ser Ala Asp Phe Gly His Pro Asp Val Phe Cys
 325 330 335
 Lys Asn Leu Pro Gly Arg Ser Trp Phe Ile Ser Ala Thr Ala Thr Val
 340 345 350
 Lys Asn Pro Gln Val Glu Pro Tyr Ile Glu Arg Leu Thr Lys Arg Asp
 355 360 365
 Leu His Asp Gly Lys Val Asn Thr Gly Gly Ile Ile Thr Val Thr Asp
 370 375 380
 Ser Asn Trp Met Leu Ser Trp Thr Ile His Arg Gln Pro His Phe Lys
 385 390 395 400
 Lys Gln Lys Lys Asn Glu Thr Ile Val Trp Ile Tyr Gly Leu Tyr Ser
 405 410 415
 Asn Thr Lys Gly Asn Tyr Ile Lys Lys Arg Ile Val Asp Cys Thr Gly
 420 425 430
 Glu Glu Ile Thr Lys Glu Trp Leu Ser Ile Trp Gly Phe Gln Lys Pro
 435 440 445
 Leu Ile Asp Asp Leu Ala Lys Glu Ser Ser Ile Asn Thr Val Pro Val
 450 455 460
 Tyr Met Pro Phe Ile Thr Ser Tyr Phe Met Pro Arg Val Lys Gly Asp
 465 470 475 480
 Arg Pro Asp Val Val Pro Glu Gly Ser Ala Asn Leu Ala Phe Ile Gly
 485 490 495
 Asn Phe Ala Glu Ser Pro Ser Arg Asp Thr Val Phe Thr Thr Glu Tyr
 500 505 510
 Ser Val Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asp Val Asp
 515 520 525
 Arg Gly Val Pro Glu Val Phe Asn Ser Ile Tyr Asp Leu Arg Glu Leu
 530 535 540
 Met Arg Ala Met Tyr Tyr Met Asn Asp Lys Lys Pro Leu Lys Asp Met
 545 550 555 560
 Asp Leu Pro Ile Pro Lys Ile Val Glu Lys Pro Leu Leu Lys Lys Leu
 565 570 575
 Gln Gly Thr Trp Ile Gly Glu Leu Met Glu Gln Gln His Leu Leu
 580 585 590

<210> 19

<211> 656

<212> DNA

<213> Lactobacillus reuteri

<220>
<221> CDS
<222> (1)..(654)

<400> 19
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Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe
1 5 10 15

gat ggt caa gaa aca cca cca tta aag atc cat caa tta ttt gat tca 96
Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
20 25 30

caa aaa tac gat cag tta atc gca gta act ggg aaa att act gct gac 144
Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
35 40 45

ttc att aat aaa tac ctt agt aat ttt atc agt att aat gta gcg tta 192
Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
50 55 60

agc tcc caa tca act agt gaa tta agt gct gat gag atg gtg aca aag 240
Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
65 70 75 80

gtt gca ctt acc aat gct ctc ctt agt tca gca aat aaa gaa gct gct 288
Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
85 90 95

aaa ctc ttc tca gcg tta acc agt gac aac caa acg aac gtc tta aat 336
Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
100 105 110

aat ctt ttt cgc gta tca atc gcg cct act cag gtt atc cat tct aag 384
Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
115 120 125

ttt tac ttg tta agt agt tca act act cat gat tcc cgt gtg att ctt 432
Phe Tyr Leu Leu Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
130 135 140

ggg agt gta gat tta gac gaa gct tca ttt gat gct cac cga aat caa 480
Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
145 150 155 160

ttt gaa gaa gta ttg gta ttt gac aat gat gtc cgc tta tac caa aac 528
Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
165 170 175

ctt act gac cac ttt aaa aag gat ttt aag cca gta ttg aag ccc ttc 576
Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe
180 185 190

ttt act atg aac cta gta aag gca gct caa aag caa gtt gag gaa gga 624
Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly
195 200 205

aag aaa gat cag gat agc ggt aag gga ccg gt 656
Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro
210 215

<210> 20
<211> 218
<212> PRT
<213> Lactobacillus reuteri

<400> 20
Met Val Met Thr Glu Thr Ala Gly Ile Arg. Lys Ile His Ile Val Phe
1 5 10 15
Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
20 25 30
Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
35 40 45
Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
50 55 60
Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
65 70 75 80
Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
85 90 95
Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
100 105 110
Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
115 120 125
Phe Tyr Leu Leu Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
130 135 140
Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
145 150 155 160
Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
165 170 175
Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe
180 185 190
Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly
195 200 205
Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro
210 215

<210> 21
<211> 726
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> CDS
<222> (1)..(726)

<220>
<221> unsure
<222> (1)..(726)
<223> n = a, c, g, or t

<400> 21

atg ctt cgt tan acc ata tta gta aaa ttg ctt att gga aga aaa cca 48
Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro
1
5
10
15

```

gtc aca acg atc aaa aaa aca tta ccg cca act cag gaa cag gct aat    96
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn
          20           25           30

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tca gtc tta act ccg gct gtt cgc caa caa ctt ggc att tca att acc 144
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr
          35           40           45
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tgg aac aaa gcc ggt gcg ttt att atc aat aat aac caa aca aat ctt      192
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu
      50          55          60

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aac gct aag att gca agt gca ccc tat gct gta aat cat ctt gac cgt 240
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg
   65           70           75           80

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caa gga agg gcg tgg caa ggt gat gcc tgg tta aac agg aca act cg 288
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg
          85           90           .           95

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tca ata tan aag ccg aaa ttt gcc aca ggg aat ggt gct acg gat tgg 336
 Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp
 100 105 110

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cga cca gct ggc ttc ctt cag gcg cat aat ctt aaa ggc ggg tac aat 384
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn
           115          120          125
```

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cat gca tac gat cgc gga cac ctt ctt gcc tat gca cta gtt ggt ggt 432
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly
130          135          140

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att cat gga ttt gat gca tcc gaa tca aat cca tct aat att gcc acg 480
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr
145 150 155 160

caa act gcc tgg gca aat gaa gca cga agt aag aac tca aca ggg caa 528
 Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln
 165 170 175

aat tac tac gaa ggt ctg gtg aga aaa gca tta gat cag aat aag caa 576
 Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln
 180 185 190

gtt cgc tac cga gtt acc aat att tat gac ggt aat aat atc gtt ccg 624
 Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro
 195 200 205 .

gca ggt gct cat atc gaa gct aaa tct agt gat ggt tct cta gaa tac 672
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
210 215 220

aat gtc ttt gtt ccg aat gtc caa aga aac att acc att aat tat tca	720		
Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser			
225	230	235	240
acc ggt	726		
Thr Gly			
<210> 22			
<211> 242			
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<213> Lactobacillus reuteri			
<220>			
<221> UNSURE			
<222> (1)..(242)			
<223> Xaa = Tyr or stop			
<400> 22			
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Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn			
20	25	30	
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr			
35	40	45	
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu			
50	55	60	
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg			
65	70	75	80
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg			
85	90	95	
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp			
100	105	110	
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn			
115	120	125	
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly			
130	135	140	
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr			
145	150	155	160
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln			
165	170	175	
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln			
180	185	190	
Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro			
195	200	205	
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr			
210	215	220	

Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
225 230 235 240

Thr Gly

<210> 23
<211> 18
<212> DNA
<213> Lactobacillus reuteri

<400> 23
aatctagtga tggttctc

18

<210> 24
<211> 18
<212> DNA
<213> Lactobacillus reuteri

<400> 24
caagttgagg aaggaaag

18

<210> 25
<211> 3684
<212> DNA
<213> Lactobacillus reuteri

<400> 25
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gaaacaacag ataagatcgc tgaaacagac atgggtggatc ttgttgaagca tgaccttcag 120
catgatattg accataatct ttgttctgaa atgatcacaa agtcaatcgc tgatattacc 180
ataaatcggt ctcaagcaaa ggagaaaatt gctaaggcagg ttaagcaaca tgatacgtt 240
tatactttgc aaaaagaagc ggtctctcct cgggcagcgtc agccaaaact aaagactcga 300
gaaaaaaatta ccaaggcagg tcaggatgct ttgatcagt gaatgtcacc acagcaacgg 360
gatgttgaga aaaagtacac gactttctg tacgatcggc caatggaaacg aaacattgcg 420
aataacaata gtggcctata cgttcctaatt gatacgggaa ctcacccaaat cccatttgg 480
aaaattgcaa ctatttctga aattcgtgac ggtttaaaga gcattgtatc tgttatgaag 540
ggctatcagc agtttgcgt tgattatgat gctgactacg ggaagcgggtt ctttgaagca 600
attttgtata gttttactgc accgtttta tgggaaattc gttctaaagc tagcctgaac 660
cctgaagatg ggaatgatgt tcctaatttc ctaatcctag gggcaacggc tggttccgg 720
aagtctaccc ttcttcggat tattaatcag ctcacgtgga acactgatcg ctctgtt 780
gactttggaa cgatctaccc gtcgcaaaact cctcaaaaga aggcaaaagac tgttgaggcg 840
atggAACATT atatgaaact tggtagttca taccgggttt tgtagatga aattgaacccg 900
tacttttcc agcaagatca atatagtcgat cttggatgtt ggtttgttat gattaagggt 960
gttacgatta ttgcaatgat tatttttgtt ttactgggtt tcgttcttgg gtttaggtat 1020
aactggcacc cagttggat ttctaatttg tggtctcatg gcgattctt taccgggtggc 1080
tttatgggct ttatgttctc gctatctgtt attgtgggtt ctatcaggg aattgagttt 1140
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tccgttatct ggcggatctt aatctctat attggtgcaa ttttcgtcat tgtttctatt 1260
tacccatgga acgaattgaa gtccgttggc tcaccattcg ttgaaacctt cacgaagggtt 1320
ggaattactg gagcagccgg aatcattaaac ttgttgggtt tgacggcgc tctttctgg 1380
gctaactctg gaattttacag tgcttagtcgg atgttggatca agctttctgt tgatggggaa 1440
gtaccaaaagt tcttttagtaa gctttccaag cgcgttggc ctaatgttgc aatcctcagc 1500
atttcttcctt ggtatcttcctt tggctttgtttaattatgaat taatgtcgat ttttagttct 1560
gctgctcaaa atatttcgtt cattgtatat agttccagtg ttcttccagg gatggatcca 1620
tggtttatca ttctcttgc agaacttcac ttcagaaaag aacaccctga acagcttaaa 1680

gatcatccat tcaagatgcc gcttacccg gcttataact actttagttt gattgccttg 1740
actgtgatct tgatcttcat gttctttaac ccagataactc gagtttcagt atcagtttgt 1800
gttatcttct tgattatcat gagtattatt tatcgttttc gtgttcatga aggaaaagaa 1860
aagtaaatat atagctaaag cagcttgc aatcctgcgt acaatacccc tttagggttga 1920
cactttaat aataaaagtg tgaatcctag ggggtgttt gcattgttaag ttattcaact 1980
attgaaaagc ttaaattact tcattgattat cagaatccgg attatggttt aacgggtgtac 2040
tccgattacc atgggtgtccg accagcaaac atgagtaagt ggattaagca attcctactc 2100
gctggattgg cgggattaaat tagacctaag cataatcaga agtactcatt agagactaag 2160
ttaactgctg taaaagctt tcttctggc aagtatacta atcaagcaat tctccagcag 2220
tatcaaatta gaaatatttc tcaactacat caatgggtt tcagttacaa taatgacaaa 2280
ctccgagttt atcagacaac gagaaagcga gtcagaaaaa tgggacgaaa agtaacctt 2340
gatgaaaaga ggcagattgt ccgatggaca attgaacata acaataacta taaagcggct 2400
gcagagaagt atgatattag ttaccaacga gtttattctt gggtaacgaa gtaccgagta 2460
aatagcgact gggtaactt aaaaagataac cgtggcgta ataaaggaaa agagccact 2520
aatgaacttag aaaaactaag gaaacgagtt cgtgagctag aagatcgtga ccgtgaacgg 2580
gagctgcaaa tcgcttcgc aaaaaaatta gtcgaaatac gcaatcgaaa ggtgaaacga 2640
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ccaaggtcgc tggtaattact agacaggctt actacaaatg gttgaaacat gaaccgacta 2760
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<210> 26
<211> 7113
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> unsure
<222> (1)..(7113)
<223> n = a, c, g, or t

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aatcaccacg tcatgcgtt gtgaaatcgt ttaagtcgt tatctggcg atcttaatct 300
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tatatagttc cagtgttctt ccagggttgc taccatggttt tatcattctc ttgtcagaac 720
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acccggctta taactactttt agtttgcattt ccttgactgt gatcttgcattt ttcatgttct 840

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cgtacttctt ccagcaagat caatataatgc gac 7020
7113

<210> 27
<211> 941
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> CDS
<222> (3)...(941)

<400> 27
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Arg Leu Glu Phe Trp Phe Ala Met Ile Lys Val Val Thr Ile Ile
1 5 10 15

gca atg att att ctt ggt tta ctg gtt atc gtt ctt ggg tta ggt aat 95

Ala Met Ile Ile Leu Gly Leu Leu Val Ile Val Leu Gly Leu Gly Asn			
20	25	30	
aac tgg cac cca gtt ggg att tct aat ttg tgg tct cat ggc gga ttc			143
Asn Trp His Pro Val Gly Ile Ser Asn Leu Trp Ser His Gly Gly Phe			
35	40	45	
ttt acc ggt ggc ttt atg ggc ttt atg ttc tcg cta tct gtg att gct			191
Phe Thr Gly Gly Phe Met Gly Phe Met Phe Ser Leu Ser Val Ile Ala			
50	55	60	
ggt tct tat cag gga att gag tta ttg gga atc act gct ggt gaa gct			239
Gly Ser Tyr Gln Gly Ile Glu Leu Leu Gly Ile Thr Ala Gly Glu Ala			
65	70	75	
gaa tca cca cgt cat gcg att gtg aaa tca gtt aag tcc gtt atc tgg			287
Glu Ser Pro Arg His Ala Ile Val Lys Ser Val Lys Ser Val Ile Trp			
80	85	90	95
cgg atc tta atc ttc tat att ggt gca att ttc gtc att gtt tct att			335
Arg Ile Leu Ile Phe Tyr Ile Gly Ala Ile Phe Val Ile Val Ser Ile			
100	105	110	
tac cca tgg aac gaa ttg aag tcc gtt ggc tca cca ttc gtt gaa acc			383
Tyr Pro Trp Asn Glu Leu Lys Ser Val Gly Ser Pro Phe Val Glu Thr			
115	120	125	
ttc acg aag gtt gga att act gga gca gcc gga atc att aac ttt gtt			431
Phe Thr Lys Val Gly Ile Thr Gly Ala Ala Gly Ile Ile Asn Phe Val			
130	135	140	
gtt ttg acg gca gct ctt tct gga gct aac tct gga att tac agt gct			479
Val Leu Thr Ala Ala Leu Ser Gly Ala Asn Ser Gly Ile Tyr Ser Ala			
145	150	155	
agt cgg atg ttg ttc aag ctt tct gtt gat ggg gaa gta cca aag ttc			527
Ser Arg Met Leu Phe Lys Leu Ser Val Asp Gly Glu Val Pro Lys Phe			
160	165	170	175
ttt agt aag ctt tcc aag cgc gtt gtt cct aat gtt gca atc ctc acg			575
Phe Ser Lys Leu Ser Lys Arg Val Val Pro Asn Val Ala Ile Leu Thr			
180	185	190	
att tct tcc tgg atc ttc ctt ggc ttt gta att aat gaa tta atg tgg			623
Ile Ser Ser Trp Ile Phe Leu Gly Phe Val Ile Asn Glu Leu Met Ser			
195	200	205	
att ttt agt tct gct gct caa aat att ttc gtc att gta tat agt tcc			671
Ile Phe Ser Ser Ala Ala Gln Asn Ile Phe Val Ile Val Tyr Ser Ser			
210	215	220	
agt gtt ctt cca ggg atg gta cca tgg ttt atc att ctc ttg tca gaa			719
Ser Val Leu Pro Gly Met Val Pro Trp Phe Ile Ile Leu Leu Ser Glu			
225	230	235	
ctt cac ttc aga aaa gaa cac cct gaa cag ctt aaa gat cat cca ttc			767
Leu His Phe Arg Lys Glu His Pro Glu Gln Leu Lys Asp His Pro Phe			
240	245	250	255
aag atg ccg ctt tac ccg gct tat aac tac ttt agt ttg att gcc ttg			815
Lys Met Pro Leu Tyr Pro Ala Tyr Asn Tyr Phe Ser Leu Ile Ala Leu			

260

265

270

act gtg atc ttg atc ttc atg ttc ttt aac cca gat act cga gtt tca 863
 Thr Val Ile Leu Ile Phe Met Phe Phe Asn Pro Asp Thr Arg Val Ser
 275 280 285

gta tca gtt ggt gtt atc ttc ttg att atc atg agt att att tat cgt 911
 Val Ser Val Gly Val Ile Phe Leu Ile Ile Met Ser Ile Ile Tyr Arg
 290 295 300

gtt cgt gtt cat gaa gga aaa gaa aag taa 941
 Val Arg Val His Glu Gly Lys Glu Lys
 305 310

<210> 28

<211> 312

<212> PRT

<213> Lactobacillus reuteri

<400> 28

Arg Leu Glu Phe Trp Phe Ala Met Ile Lys Val Val Thr Ile Ile Ala
 1 5 10 15
 Met Ile Ile Leu Gly Leu Leu Val Ile Val Leu Gly Leu Gly Asn Asn
 20 25 30
 Trp His Pro Val Gly Ile Ser Asn Leu Trp Ser His Gly Gly Phe Phe
 35 40 45
 Thr Gly Gly Phe Met Gly Phe Met Phe Ser Leu Ser Val Ile Ala Gly
 50 55 60
 Ser Tyr Gln Gly Ile Glu Leu Leu Gly Ile Thr Ala Gly Glu Ala Glu
 65 70 75 80
 Ser Pro Arg His Ala Ile Val Lys Ser Val Lys Ser Val Ile Trp Arg
 85 90 95
 Ile Leu Ile Phe Tyr Ile Gly Ala Ile Phe Val Ile Val Ser Ile Tyr
 100 105 110
 Pro Trp Asn Glu Leu Lys Ser Val Gly Ser Pro Phe Val Glu Thr Phe
 115 120 125
 Thr Lys Val Gly Ile Thr Gly Ala Ala Gly Ile Ile Asn Phe Val Val
 130 135 140
 Leu Thr Ala Ala Leu Ser Gly Ala Asn Ser Gly Ile Tyr Ser Ala Ser
 145 150 155 160
 Arg Met Leu Phe Lys Leu Ser Val Asp Gly Glu Val Pro Lys Phe Phe
 165 170 175
 Ser Lys Leu Ser Lys Arg Val Val Pro Asn Val Ala Ile Leu Thr Ile
 180 185 190
 Ser Ser Trp Ile Phe Leu Gly Phe Val Ile Asn Glu Leu Met Ser Ile
 195 200 205
 Phe Ser Ser Ala Ala Gln Asn Ile Phe Val Ile Val Tyr Ser Ser Ser
 210 215 220
 Val Leu Pro Gly Met Val Pro Trp Phe Ile Ile Leu Leu Ser Glu Leu
 225 230 235 240
 His Phe Arg Lys Glu His Pro Glu Gln Leu Lys Asp His Pro Phe Lys
 245 250 255
 Met Pro Leu Tyr Pro Ala Tyr Asn Tyr Phe Ser Leu Ile Ala Leu Thr
 260 265 270
 Val Ile Leu Ile Phe Met Phe Phe Asn Pro Asp Thr Arg Val Ser Val
 275 280 285
 Ser Val Gly Val Ile Phe Leu Ile Ile Met Ser Ile Ile Tyr Arg Val
 290 295 300
 Arg Val His Glu Gly Lys Glu Lys
 305 310

<210> 29
 <211> 600
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(597)

<400> 29

atg agt aag tgg att aag caa ttc cta ctc gct gga ttg gcg gga tta Met Ser Lys Trp Ile Lys Gln Phe Leu Leu Ala Gly Leu Ala Gly Leu	48
1 5 10 15	
att aga cct aag cat aat cag aag tac tca tta gag act aag tta act Ile Arg Pro Lys His Asn Gln Lys Tyr Ser Leu Glu Thr Lys Leu Thr	96
20 25 30	
gct gta aaa gct tat ctt tct ggc aag tat act aat caa gca att ctc Ala Val Lys Ala Tyr Leu Ser Gly Lys Tyr Thr Asn Gln Ala Ile Leu	144
35 40 45	
cag cag tat caa att aga aat att tct caa cta cat caa tgg gtt atc Gln Gln Tyr Gln Ile Arg Asn Ile Ser Gln Leu His Gln Trp Val Ile	192
50 55 60	
agt tac aat aat gac aaa ctc cga gtt aat cag aca acg aga aag cga Ser Tyr Asn Asn Asp Lys Leu Arg Val Asn Gln Thr Thr Arg Lys Arg	240
65 70 75 80	
gtc aga aaa atg gga cga aaa gta acc ttt gat gaa aag agg cag att Val Arg Lys Met Gly Arg Lys Val Thr Phe Asp Glu Lys Arg Gln Ile	288
85 90 95	
gtc cga tgg aca att gaa cat aac aat aac tat aaa gcg gct gca gag Val Arg Trp Thr Ile Glu His Asn Asn Tyr Lys Ala Ala Glu	336
100 105 110	
aag tat gat att agt tac caa cga gtt tat tct tgg gta cgg aag tac Lys Tyr Asp Ile Ser Tyr Gln Arg Val Tyr Ser Trp Val Arg Lys Tyr	384
115 120 125	
cga gta aat agc gac tgg gaa gta cta aaa gat aac cgt ggg cgt aat Arg Val Asn Ser Asp Trp Glu Val Leu Lys Asp Asn Arg Gly Arg Asn	432
130 135 140	
aaa gga aaa gag ccc act aat gaa cta gaa aaa cta agg aaa cga gtt Lys Gly Lys Glu Pro Thr Asn Glu Leu Glu Lys Leu Arg Lys Arg Val	480
145 150 155 160	
cgt gag cta gaa gat cgt gac cgt gaa cgg gag ctg caa atc gct ttc Arg Glu Leu Glu Asp Arg Asp Arg Glu Arg Glu Leu Gln Ile Ala Phe	528
165 170 175	
gca aaa aaa tta gtc gaa ata cgc aat cgg gag gtg aaa cga ccg gac Ala Lys Lys Leu Val Glu Ile Arg Asn Arg Glu Val Lys Arg Pro Asp	576
180 185 190	

gat atc aag cga ttc aag aaa tga 600
Asp Ile Lys Arg Phe Lys Lys
195

<210> 30
<211> 199
<212> PRT
<213> Lactobacillus reuteri

<400> 30
Met Ser Lys Trp Ile Lys Gln Phe Leu Leu Ala Gly Leu Ala Gly Leu
1 5 10 15

Ile Arg Pro Lys His Asn Gln Lys Tyr Ser Leu Glu Thr Lys Leu Thr
20 25 30

Ala Val Lys Ala Tyr Leu Ser Gly Lys Tyr Thr Asn Gln Ala Ile Leu
35 40 45

Gln Gln Tyr Gln Ile Arg Asn Ile Ser Gln Leu His Gln Trp Val Ile
50 55 60

Ser Tyr Asn Asn Asp Lys Leu Arg Val Asn Gln Thr Thr Arg Lys Arg
65 70 75 80

Val Arg Lys Met Gly Arg Lys Val Thr Phe Asp Glu Lys Arg Gln Ile
85 90 95

Val Arg Trp Thr Ile Glu His Asn Asn Tyr Lys Ala Ala Ala Glu
100 105 110

Lys Tyr Asp Ile Ser Tyr Gln Arg Val Tyr Ser Trp Val Arg Lys Tyr
115 120 125

Arg Val Asn Ser Asp Trp Glu Val Leu Lys Asp Asn Arg Gly Arg Asn
130 135 140

Lys Gly Lys Glu Pro Thr Asn Glu Leu Glu Lys Leu Arg Lys Arg Val
145 150 155 160

Arg Glu Leu Glu Asp Arg Asp Arg Glu Arg Glu Leu Gln Ile Ala Phe
165 170 175

Ala Lys Lys Leu Val Glu Ile Arg Asn Arg Glu Val Lys Arg Pro Asp
180 185 190

Asp Ile Lys Arg Phe Lys Lys
195

<210> 31
<211> 849
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> CDS
<222> (1)...(849)

<400> 31

atg aac aat gaa ggt tat tcc att agt gaa ttg gcc aag gtc gct gga Met Asn Asn Glu Gly Tyr Ser Ile Ser Glu Leu Ala Lys Val Ala Gly	48
1 5 10 15	
att act aga cag gct tac tac aaa tgg ttg aaa cat gaa ccg act aaa Ile Thr Arg Gln Ala Tyr Tyr Lys Trp Leu Lys His Glu Pro Thr Lys	96
20 25 30	
tat gag att gaa gaa tcg gag att ctc caa ttg att aaa cag tta gaa Tyr Glu Ile Glu Glu Ser Glu Ile Leu Gln Leu Ile Lys Gln Leu Glu	144
35 40 45	
aat gaa cat aag caa agc gtt ggt tat gac aaa atg act agg tta atc Asn Glu His Lys Gln Ser Val Gly Tyr Asp Lys Met Thr Arg Leu Ile	192
50 55 60	
aag tta agt cag cag atc tct tat acc gtt aat aag aaa cga gtc att Lys Leu Ser Gln Gln Ile Ser Tyr Thr Val Asn Lys Lys Arg Val Ile	240
65 70 75 80	
cgt att atg aaa ggc cat agt atc aag gcc gac tat cgt cag cca acc Arg Ile Met Lys Gly His Ser Ile Lys Ala Asp Tyr Arg Gln Pro Thr	288
85 90 95	
gac aaa cgt att caa gcc cag caa act tat gaa gct gaa aat att ctt Asp Lys Arg Ile Gln Ala Gln Gln Thr Tyr Glu Ala Glu Asn Ile Leu	336
100 105 110	
aac cga caa ttt gac caa act gca gct aac caa gtt tgg gtt acg gat Asn Arg Gln Phe Asp Gln Thr Ala Ala Asn Gln Val Trp Val Thr Asp	384
115 120 125	
acg acg gaa ctg aat tac gga atc tgg ctt aat aaa gtt cgt cta cat Thr Thr Glu Leu Asn Tyr Gly Ile Trp Leu Asn Lys Val Arg Leu His	432
130 135 140	
ata gta tta gat tta tat ggt caa tac cca gta agc tgg tta att aca Ile Val Leu Asp Leu Tyr Gly Gln Tyr Pro Val Ser Trp Leu Ile Thr	480
145 150 155 160	
cct aca gaa acc gct gaa gga gta gtt caa gtg ttc gag caa gca cggt Pro Thr Glu Thr Ala Glu Gly Val Val Gln Val Phe Glu Gln Ala Arg	528
165 170 175	
atg aaa gaa gga gca cta gct ccg tta att cat act gat cgt ggt gcg Met Lys Glu Gly Ala Leu Ala Pro Leu Ile His Thr Asp Arg Gly Ala	576
180 185 190	
gcg tat act tcc aaa gca ttt aat cag tat tta gta gtt aat ggt gcc Ala Tyr Thr Ser Lys Ala Phe Asn Gln Tyr Leu Val Val Asn Gly Ala	624
195 200 205	
caa cac agt tat tca gca cca ggg aca ccg gct gac aat gcc gta ata Gln His Ser Tyr Ser Ala Pro Gly Thr Pro Ala Asp Asn Ala Val Ile	672
210 215 220	
gaa cat tgg tgg gca gat ttt aag gct att tgg atc gca cat cta cct Glu His Trp Trp Ala Asp Phe Lys Ala Ile Trp Ile Ala His Leu Pro	720
225 230 235 240	

aaa gca caa aca tta tta gaa cta gaa gaa caa gtt aga gaa gga att 768
Lys Ala Gln Thr Leu Leu Glu Leu Glu Gln Val Arg Glu Gly Ile
245 250 255

acc tat ttc act gaa aaa ttt atc tca gcg aag aga aat gac ctt acc 816
Thr Tyr Phe Thr Glu Lys Phe Ile Ser Ala Lys Arg Asn Asp Leu Thr
260 265 270

gca gcg gaa tac cgc ttt ggc aag gcc aac taa 849
Ala Ala Glu Tyr Arg Phe Gly Lys Ala Asn
275 280

<210> 32

<211> 282

<212> PRT

<213> Lactobacillus reuteri

<400> 32

Met Asn Asn Glu Gly Tyr Ser Ile Ser Glu Leu Ala Lys Val Ala Gly
1 5 10 15
Ile Thr Arg Gln Ala Tyr Tyr Lys Trp Leu Lys His Glu Pro Thr Lys
20 25 30
Tyr Glu Ile Glu Glu Ser Glu Ile Leu Gln Leu Ile Lys Gln Leu Glu
35 40 45
Asn Glu His Lys Gln Ser Val Gly Tyr Asp Lys Met Thr Arg Leu Ile
50 55 60
Lys Leu Ser Gln Gln Ile Ser Tyr Thr Val Asn Lys Lys Arg Val Ile
65 70 75 80
Arg Ile Met Lys Gly His Ser Ile Lys Ala Asp Tyr Arg Gln Pro Thr
85 90 95
Asp Lys Arg Ile Gln Ala Gln Gln Thr Tyr Glu Ala Glu Asn Ile Leu
100 105 110
Asn Arg Gln Phe Asp Gln Thr Ala Ala Asn Gln Val Trp Val Thr Asp
115 120 125
Thr Thr Glu Leu Asn Tyr Gly Ile Trp Leu Asn Lys Val Arg Leu His
130 135 140
Ile Val Leu Asp Leu Tyr Gly Gln Tyr Pro Val Ser Trp Leu Ile Thr
145 150 155 160
Pro Thr Glu Thr Ala Glu Gly Val Val Gln Val Phe Glu Gln Ala Arg
165 170 175
Met Lys Glu Gly Ala Leu Ala Pro Leu Ile His Thr Asp Arg Gly Ala
180 185 190
Ala Tyr Thr Ser Lys Ala Phe Asn Gln Tyr Leu Val Val Asn Gly Ala
195 200 205
Gln His Ser Tyr Ser Ala Pro Gly Thr Pro Ala Asp Asn Ala Val Ile
210 215 220
Glu His Trp Trp Ala Asp Phe Lys Ala Ile Trp Ile Ala His Leu Pro
225 230 235 240
Lys Ala Gln Thr Leu Leu Glu Leu Glu Gln Val Arg Glu Gly Ile
245 250 255
Thr Tyr Phe Thr Glu Lys Phe Ile Ser Ala Lys Arg Asn Asp Leu Thr
260 265 270
Ala Ala Glu Tyr Arg Phe Gly Lys Ala Asn
275 280

<210> 33

<211> 744

<212> DNA

<213> Lactobacillus reuteri

<220>

<221> CDS

<222> (1)..(744)

<220>

<221> unsure

<222> (1)..(744)

<223> n = a, c, g, or t

<400> 33

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Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro
1 5 10 15

gtc aca acg atc aaa aaa aca tta ccg cca act cag gaa cag gct aat 96
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn
20 25 30

tca gtc tta act ccg gct gtt cgc caa caa ctt ggc att tca att acc 144
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr
35 40 45

tgg aac aaa gcc ggt gcg ttt att atc aat aat aac caa aca aat ctt 192
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Gln Thr Asn Leu
50 55 60

aac gct aag att gca agt gca ccc tat gct gta aat cat ctt gac cgt 240
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg
65 70 75 80

caa gga agg gcg tgg caa ggt gat gcc tgg tta aac agg aca act ccg 288
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg
85 90 95

tca ata tan aag ccg aaa ttt gcc aca ggg aat ggt gct acg gat tgg 336
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp
100 105 110

cga cca gct ggc ttc ctt cag gcg cat aat ctt aaa ggc ggg tac aat 384
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn
115 120 125

cat gca tac gat cgc gga cac ctt ctt gcc tat gca cta gtt ggt ggt 432
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly
130 135 140

att cat gga ttt gat gca tcc gaa tca aat cca tct aat att gcc acg 480
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr
145 150 155 160

caa act gcc tgg gca aat gaa gca cga agt aag aac tca aca ggg caa 528
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln
165 170 175

aat tac tac gaa ggt ctg gtg aga aaa gca tta gat cag aat aag caa 576
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln
180 185 190

gtt cgc tac cga gtt acc aat att tat gac ggt aat aat atc gtt ccg 624

Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro			
195	200	205	
gca ggt gct cat atc gaa gct aaa tct agt gat ggt tct cta gaa tac			672
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr			
210	215	220	
aat gtc ttt gtt ccg aat gtc caa aga aac att acc att aat tat tca			720
Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser			
225	230	235	240
acc ggt gca gta aaa caa aac taa			744
Thr Gly Ala Val Lys Gln Asn			
245			
<210> 34			
<211> 247			
<212> PRT			
<213> Lactobacillus reuteri			
<220>			
<221> UNSURE			
<222> (1)..(247)			
<223> Xaa = Tyr or stop			
<400> 34			
Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro			
1 5 10 15			
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn			
20 25 30			
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr			
35 40 45			
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu			
50 55 60			
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg			
65 70 75 80			
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg			
85 90 95			
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp			
100 105 110			
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn			
115 120 125			
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly			
130 135 140			
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr			
145 150 155 160			
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln			
165 170 175			
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln			
180 185 190			
Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro			
195 200 205			
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr			
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Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser			
225 230 235			240
Thr Gly Ala Val Lys Gln Asn			
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<212> DNA
<213> Lactobacillus reuteri
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<220>
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 1 5 10 15

 gat ggt caa gaa aca cca cca tta aag atc cat caa tta ttt gat tca 96
 Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
 20 25 30

 caa aaa tac gat cag tta atc gca gta act ggg aaa att act gct gac 144
 Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
 35 40 45

 ttc att aat aaa tac ctt agt aat ttt atc agt att aat gta gcg tta 192
 Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
 50 55 60

 agc tcc caa tca act agt gaa tta agt gct gat gag atg gtg aca aag 240
 Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
 65 70 75 80

 gtt gca ctt acc aat gct ctc ctt agt tca gca aat aaa gaa gct gct 288
 Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
 85 90 95

 aaa ctc ttc tca gcg tta acc agt gac aac caa acg aac gtc tta aat 336
 Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
 100 105 110

 aat gtt ttt cgc gta tca atc gcg cct act cag gtt atc cat tct aag 384
 Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
 115 120 125

 ttt tac ttg tta agt agt tca act act cat gat tcc cgt gtg att ctt 432
 Phe Tyr Leu Leu Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
 130 135 140

 ggg agt gta gat tta gac gaa gct tca ttt gat gct cac cga aat caa 480
 Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
 145 150 155 160

 ttt gaa gaa gta ttg gta ttt gac aat gat gtc cgc tta tac caa aac 528
 Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
 165 170 175

 ctt act gac cac ttt aaa aag gat ttt aag cca gta ttg aag ccc ttc 576
 Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe
 180 185 190

 ttt act atg aac cta gta aag gca gct caa aag caa gtt gag gaa gga 624
 Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly

195	200	205	
aag aaa gat cag gat agc ggt aag gga ccg gtt atc ctt gat aat gaa Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro Val Ile Leu Asp Asn Glu 210 215 220			672
aca aca gat aag atc gct gaa aca gac atg gtg gat ctg ttg aag cat Thr Thr Asp Lys Ile Ala Glu Thr Asp Met Val Asp Leu Leu Lys His 225 230 235 240			720
gac ctt cag cat gat att gac cat aat ctt gtt cct gaa atg atc aca Asp Leu Gln His Asp Ile Asp His Asn Leu Val Pro Glu Met Ile Thr 245 250 255			768
aag tca atg cgt gat att acc ata aat cgt tct caa gca aag gag aaa Lys Ser Met Arg Asp Ile Thr Ile Asn Arg Ser Gln Ala Lys Glu Lys 260 265 270			816
att gct aag cag gtt aag caa cat gat acg att tat act ttg caa aaa Ile Ala Lys Gln Val Lys Gln His Asp Thr Ile Tyr Thr Leu Gln Lys 275 280 285			864
gaa gcg gtc tct cct cg ^g gca gct aag cca aaa cta aag act cga gaa Glu Ala Val Ser Pro Arg Ala Ala Lys Pro Lys Leu Lys Thr Arg Glu 290 295 300			912
aaa att acc aag cag gtt cag gat gct ttg atc agt gga atg tca cca Lys Ile Thr Lys Gln Val Gln Asp Ala Leu Ile Ser Gly Met Ser Pro 305 310 315 320			960
cag caa cg ^g gat gct gag aaa aag tac acg act ttt ctg tac gat cg ^g Gln Gln Arg Asp Ala Glu Lys Lys Tyr Thr Thr Phe Leu Tyr Asp Arg 325 330 335			1008
cca atg gaa cga aac att gc ^g aat aac aat agt ggc cta tac gtt cct Pro Met Glu Arg Asn Ile Ala Asn Asn Ser Gly Leu Tyr Val Pro 340 345 350			1056
aat gat acg gga act cac cca atc cca ttt ggt aaa att gca act att Asn Asp Thr Gly Thr His Pro Ile Pro Phe Gly Lys Ile Ala Thr Ile 355 360 365			1104
tct gaa att cgt gac ggt tta aag agc att gat gct gtt atg aag ggc Ser Glu Ile Arg Asp Gly Leu Lys Ser Ile Asp Ala Val Met Lys Gly 370 375 380			1152
tat cag cag ttt gtc gtt gat tat gat gct gac tac ggg aag cg ^g ttc Tyr Gln Gln Phe Val Val Asp Tyr Asp Ala Asp Tyr Gly Lys Arg Phe 385 390 395 400			1200
ttt gaa gca att ttg tat agt ttt act gca ccg ttt tta tgg gaa att Phe Glu Ala Ile Leu Tyr Ser Phe Thr Ala Pro Phe Leu Trp Glu Ile 405 410 415			1248
cgt tct aaa gct agc ctg aac cct gaa gat ggg aat gat gtt cct aat Arg Ser Lys Ala Ser Leu Asn Pro Glu Asp Gly Asn Asp Val Pro Asn 420 425 430			1296
ttc cta atc cta ggg gca acg gct ggt tcc gga aag tct acc ctt ctt Phe Leu Ile Leu Gly Ala Thr Ala Gly Ser Gly Lys Ser Thr Leu Leu 435 440 445			1344

cgg att att aat cag ctc acg tgg aac act gat cgc tcg ttg att gac		1392	
Arg Ile Ile Asn Gln Leu Thr Trp Asn Thr Asp Arg Ser Leu Ile Asp			
450	455	460	
ttt gga acg atc tac ccg tcg caa act cct caa aag aag gca aag act		1440	
Phe Gly Thr Ile Tyr Pro Ser Gln Thr Pro Gln Lys Lys Ala Lys Thr			
465	470	475	480
gtt gag gcg atg gaa cat tat atg aaa ctt ggt agt tca tac ccg gtt		1488	
Val Glu Ala Met Glu His Tyr Met Lys Leu Gly Ser Ser Tyr Pro Val			
485	490	495	
ttg tta gat gaa att gaa ccg tac ttc ttc cag caa gat caa tat agt		1536	
Leu Leu Asp Glu Ile Glu Pro Tyr Phe Phe Gln Gln Asp Gln Tyr Ser			
500	505	510	
cga c		1540	
Arg			

<210> 36

<211> 513

<212> PRT

<213> Lactobacillus reuteri

<400> 36

Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe			
1	5	10	15

Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser		
20	25	30

Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp		
35	40	45

Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu		
50	55	60

Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys			
65	70	75	80

Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala		
85	90	95

Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn		
100	105	110

Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys		
115	120	125

Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu		
130	135	140

Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln			
145	150	155	160

Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn		
165	170	175

Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe

180

185

190

Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly
195 200 205

Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro Val Ile Leu Asp Asn Glu
210 215 220

Thr Thr Asp Lys Ile Ala Glu Thr Asp Met Val Asp Leu Leu Lys His
225 230 235 240

Asp Leu Gln His Asp Ile Asp His Asn Leu Val Pro Glu Met Ile Thr
245 250 255

Lys Ser Met Arg Asp Ile Thr Ile Asn Arg Ser Gln Ala Lys Glu Lys
260 265 270

Ile Ala Lys Gln Val Lys Gln His Asp Thr Ile Tyr Thr Leu Gln Lys
275 280 285

Glu Ala Val Ser Pro Arg Ala Ala Lys Pro Lys Leu Lys Thr Arg Glu
290 295 300

Lys Ile Thr Lys Gln Val Gln Asp Ala Leu Ile Ser Gly Met Ser Pro
305 310 315 320

Gln Gln Arg Asp Ala Glu Lys Lys Tyr Thr Thr Phe Leu Tyr Asp Arg
325 330 335

Pro Met Glu Arg Asn Ile Ala Asn Asn Ser Gly Leu Tyr Val Pro
340 345 350

Asn Asp Thr Gly Thr His Pro Ile Pro Phe Gly Lys Ile Ala Thr Ile
355 360 365

Ser Glu Ile Arg Asp Gly Leu Lys Ser Ile Asp Ala Val Met Lys Gly
370 375 380

Tyr Gln Gln Phe Val Val Asp Tyr Asp Ala Asp Tyr Gly Lys Arg Phe
385 390 395 400

Phe Glu Ala Ile Leu Tyr Ser Phe Thr Ala Pro Phe Leu Trp Glu Ile
405 410 415

Arg Ser Lys Ala Ser Leu Asn Pro Glu Asp Gly Asn Asp Val Pro Asn
420 425 430

Phe Leu Ile Leu Gly Ala Thr Ala Gly Ser Gly Lys Ser Thr Leu Leu
435 440 445

Arg Ile Ile Asn Gln Leu Thr Trp Asn Thr Asp Arg Ser Leu Ile Asp
450 455 460

Phe Gly Thr Ile Tyr Pro Ser Gln Thr Pro Gln Lys Lys Ala Lys Thr
465 470 475 480

Val Glu Ala Met Glu His Tyr Met Lys Leu Gly Ser Ser Tyr Pro Val
485 490 495

Leu Leu Asp Glu Ile Glu Pro Tyr Phe Phe Gln Gln Asp Gln Tyr Ser
500 505 510

Arg

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<210> 37
<211> 26
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> terminator
<222> (1)...(26)

<400> 37
aaagaagctg aaatttcggc ttcttt

26

<210> 38
<211> 28
<212> DNA
<213> Lactobacillus reuteri

<400> 38
gcagtcgacg gagttaagac tgaattag

28

<210> 39
<211> 26
<212> DNA
<213> Lactobacillus reuteri

<400> 39
ctagtcgacg cagttctgt catgac

26

<210> 40
<211> 32
<212> DNA
<213> Lactobacillus reuteri

<400> 40
catatgtatt attcaaacgg gaattatgaa gc

32

<210> 41
<211> 30
<212> DNA
<213> Lactobacillus reuteri

<400> 41
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30

<210> 42
<211> 35
<212> PRT
<213> Propionibacterium acnes

<220>

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<222> (30)

<223> Xaa = any amino acid

<400> 42

Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro Ala
1 5 10 15

Gly Leu Ala Ala Gly Met Tyr Leu Trp Gln Ala Gly Phe Xaa Asp Tyr
20 25 30

Thr Ile Leu
35

<210> 43

<211> 21

<212> PRT

<213> Clostridium sporogenes

<220>

<221> UNSURE

<222> (18)

<223> Xaa = any amino acid

<400> 43

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1 5 10 15

Pro Xaa Glu Ile Gln
20

<210> 44

<211> 14

<212> PRT

<213> Propionibacterium acnes

<400> 44

Lys Tyr Leu Asp Phe Val Thr Met Met Ser Phe Ala Lys Gly
1 5 10

<210> 45

<211> 9

<212> PRT

<213> Propionibacterium acnes

<400> 45

Lys Asp Leu Val Thr Arg Phe Phe Val
1 5

<210> 46

<211> 15

<212> PRT

<213> Propionibacterium acnes

<220>

<221> UNSURE

<222> (2)

<223> Xaa = Ile or Ser

<220>

<221> UNSURE

<222> (4)

<223> Xaa = His or Phe

<220>

<221> UNSURE

<222> (6)

<223> Xaa = Glu or Gln

<220>

<221> UNSURE

<222> (10)

<223> Xaa = Asp or Thr

<220>

<221> UNSURE

<222> (12)

<223> Xaa = Gly or Ser

<400> 46

Lys Xaa Ile Xaa Gln Xaa Tyr Met Val Xaa Ala Xaa Leu Val Lys
1 5 10 15

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> unsure

<222> (1)..(20)

<223> n = a, c, g, or t

<400> 47

atcgcgatna tnggngcngg

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> unsure

<222> (1)..(20)

<223> n = a, c, g, or t

<400> 48

ccngcytgcc anarrtacat

20

<210> 49
<211> 62
<212> DNA
<213> Propionibacterium acnes

<400> 49
atcgagatva trggggctgg cccggccggg ctggctgccg gaatgtacct ctggcargcs 60
gg 62

<210> 50
<211> 21
<212> PRT
<213> Propionibacterium acnes

<220>
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<222> (2)
<223> xaa = ala or glu

<220>
<221> UNSURE
<222> (3)..(4)
<223> xaa = ile or met

<400> 50
Ile Xaa Xaa Xaa Gly Ala Gly Pro Ala Gly Leu Ala Ala Gly Met Tyr
1 5 10 15

Leu Trp Gln Ala Gly
20

<210> 51
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> unsure
<222> (1)..(17)
<223> n = a, c, g, or t

<400> 51
gggccagccc cyatnat 17

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 52
gctggctgcc ggaatgtta 18

<210> 53
<211> 569
<212> DNA
<213> Propionibacterium acnes

<400> 53
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ggccaaaggag ctggcagcac atctcgatga gatggcacgt ggtcggcgaa ctgccccgtg 180
agatgttcg cgacacctatac cattaccgac cccattcatc gccaactta ttcaccacta 240
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cgttatgaga tggggccat catggcgctc cccagttacg acaccatcca ggagatcatg 480
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ggcgagatct acgtccccgaa aaaggatcc 569

<210> 54
<211> 104
<212> PRT
<213> Propionibacterium acnes

<400> 54
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Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
20 25 30
Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
35 40 45
Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
50 55 60
Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
65 70 75 80
Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
85 90 95
Ile Tyr Val Pro Glu Lys Asp Pro
100

<210> 55
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 55
cgatgtcggtc gtggtag

17

<210> 56
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 56
tcacgtatcg ccatcatc 18

<210> 57
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 57
aatccggcct gttcgag 17

<210> 58
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 58
aggacggcga gatctac 17

<210> 59
<211> 5275
<212> DNA
<213> Propionibacterium acnes

<400> 59

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gttcctgcac gaggacggcg agatctacgt cccggaaaag gatccagtgc gtggtccgca 3060
ggtcatggca gcagtgcaga agctggcca tttgctcgcc acgaagtacc agggatatga 3120
cgccaaacggc cactacaaca aggttacgaa ggacctcatg ctggccctcg acgagttct 3180
cgccctcaac gggtgcgagg cccggggaga cctgtggatc aacccttca cggcccttcgg 3240
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catgatgtcc ttgccaagg gagatctgtg gacgtggcc gacggcaccc aggcgtatgtt 3360
cgagcacctc aacggccaccc tggagcaccc ggccgaacgc aacgttgaca tcactcgcat 3420
caccggcgag gacggcaagg tccacattca caccacggac tggatcgcc agtccgacgt 3480
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cgaaactgcg gacgcgtcaga caaccccttc gatgttgc tggaaaccg gtcggccat 4560
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agagcttggt ggtgtatcc tgaatatgcac gggcgacttgc tttgagcttgc tttctgtgg 4860
ctcgccatc gtcgcgcacaaa gggggatc cggccaccgtt ggcgcacgtt atgcgcacat 4920

aggcttgtgc gccgcaacga tcacaacggc ccgcagtgg aagggttgg tggtcgatca 4980
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 cgctatcgct ggaatgttct catacgatc gaaagatgg tggctgggg cgaacacgg 5100
 gcccggattc cgtgtcgatc gctgtcgata agctgccacc gtgaccatgg acaacatctc 5160
 gacctcatca gccaacagct cggaaacgcc acgtggtaag ggcgataccg tgccgacggc 5220
 gtcgactagc cgggagtagc ggcgcaagaa tttattggtg ttggaggggc tcgag 5275

<210> 60

<211> 1275

<212> DNA

<213> Propionibacterium acnes

<220>

<221> CDS

<222> (1)..(1272)

<400> 60

atg tcc atc tcg aag gat tca cgt atc gcc atc atc ggg gct ggc ccg	48
Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro	
1 5 10 15	

gcc ggg ctg gct gcc gga atg tac ctc gaa cag gcc gga ttt cac gac	96
Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp	
20 25 30	

tac acg atc ctg gaa cgc acc gac cac gtc gga ggc aag tgc cac tca	144
Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser	
35 40 45	

ccg aac tac cac ggc cgt cgt tat gag atg ggg gcc atc atg ggc gtc	192
Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val	
50 55 60	

ccc agt tac gac acc atc cag gag atc atg gat cgc act ggc gac aag	240
Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys	
65 70 75 80	

gtc gac ggg ccg aaa ctg cgt cgc gag ttc ctg cac gag gac ggc gag	288
Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu	
85 90 95	

atc tac gtc ccg gaa aag gat cca gtg cgt ggt ccg cag gtc atg gca	336
Ile Tyr Val Pro Glu Lys Asp Pro Val Arg Gly Pro Gln Val Met Ala	
100 105 110	

gca gtg cag aag ctg ggc cag ttg ctc gcg acg aag tac cag gga tat	384
Ala Val Gln Lys Leu Gly Gln Leu Leu Ala Thr Lys Tyr Gln Gly Tyr	
115 120 125	

gac gcc aac ggc cac tac aac aag gtt cac gag gac ctc atg ctg ccc	432
Asp Ala Asn Gly His Tyr Asn Lys Val His Glu Asp Leu Met Leu Pro	
130 135 140	

ttc gac gag ttc ctc gcc ctc aac ggg tgc gag gcc gcc cga gac ctg	480
Phe Asp Glu Phe Leu Ala Leu Asn Gly Cys Glu Ala Ala Arg Asp Leu	
145 150 155 160	

tgg atc aac ccc ttc acg gcc ttc ggc tac ggg cac ttc gac aac gtc	528
Trp Ile Asn Pro Phe Thr Ala Phe Gly Tyr Gly His Phe Asp Asn Val	
165 170 175	

ccg gcc gcc tac gtg ctg aag tac ctc gac ttc gtc acc atg atg tcc Pro Ala Ala Tyr Val Leu Lys Tyr Leu Asp Phe Val Thr Met Met Ser 180 185 190	576
ttt gcc aag gga gat ctg tgg acg tgg gcc gac ggc acc cag gcg atg Phe Ala Lys Gly Asp Leu Trp Thr Trp Ala Asp Gly Thr Gln Ala Met 195 200 205	624
ttc gag cac ctc aac gcc acc ctg gag cac ccg gcc gaa cgc aac gtt Phe Glu His Leu Asn Ala Thr Leu Glu His Pro Ala Glu Arg Asn Val 210 215 220	672
gac atc act cgc atc acc cgc gag gac ggc aag gtc cac att cac acc Asp Ile Thr Arg Ile Thr Arg Glu Asp Gly Lys Val His Ile His Thr 225 230 235 240	720
acg gac tgg gat cgc gag tcc gac gtc ctc gtc acc gtc ccg ctg Thr Asp Trp Asp Arg Glu Ser Asp Val Leu Val Leu Thr Val Pro Leu 245 250 255	768
gaa aag ttc ctc gac tac tcc gac gcg gac gat gac gag cgg gag tac Glu Lys Phe Leu Asp Tyr Ser Asp Ala Asp Asp Glu Arg Glu Tyr 260 265 270	816
ttc tcg aag atc atc cac cag cag tac atg gtc gat gcc tgc ctg gtg Phe Ser Lys Ile Ile His Gln Gln Tyr Met Val Asp Ala Cys Leu Val 275 280 285	864
aag gag tac ccg acc atc tcc ggg tac gtc ccc gac aac atg agg ccc Lys Glu Tyr Pro Thr Ile Ser Gly Tyr Val Pro Asp Asn Met Arg Pro 290 295 300	912
gaa cgt ctc ggg cac gtc atg gtt tac tac cac cgc tgg gct gat gat Glu Arg Leu Gly His Val Met Val Tyr Tyr His Arg Trp Ala Asp Asp 305 310 315 320	960
ccg cac cag atc atc acg acc tac ctg cta cgt aac cat ccg gac tac Pro His Gln Ile Ile Thr Thr Tyr Leu Leu Arg Asn His Pro Asp Tyr 325 330 335	1008
gcg gac aag act cag gag gag tgc cgc cag atg gtc ctc gac gac atg Ala Asp Lys Thr Gln Glu Glu Cys Arg Gln Met Val Leu Asp Asp Met 340 345 350	1056
gag acc ttc ggt cat ccg gtc gag aag atc atc gag gag cag acc tgg Glu Thr Phe Gly His Pro Val Glu Lys Ile Ile Glu Glu Gln Thr Trp 355 360 365	1104
tac tac ttc ccg cac gtt agc tcg gag gac tac aag gcc ggg tgg tac Tyr Tyr Phe Pro His Val Ser Ser Glu Asp Tyr Lys Ala Gly Trp Tyr 370 375 380	1152
gag aag gtc gag gga atg cag ggt cgt cgc aac acc ttc tac gcc gga Glu Lys Val Glu Gly Met Gln Gly Arg Arg Asn Thr Phe Tyr Ala Gly 385 390 395 400	1200
gaa att atg agt ttc ggt aat ttc gac gag gtc ctc cac tac tcg aag Glu Ile Met Ser Phe Gly Asn Phe Asp Glu Val Cys His Tyr Ser Lys 405 410 415	1248

gac ctg gtg acg cgg ttc ttc gtg tga
Asp Leu Val Thr Arg Phe Phe Val
420

1275

<210> 61

<211> 424

<212> PRT

<213> Propionibacterium acnes

<400> 61

Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
1 5 10 15

Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
20 25 30

Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
35 40 45

Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
50 55 60

Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
65 70 75 80

Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
85 90 95

Ile Tyr Val Pro Glu Lys Asp Pro Val Arg Gly Pro Gln Val Met Ala
100 105 110

Ala Val Gln Lys Leu Gly Gln Leu Leu Ala Thr Lys Tyr Gln Gly Tyr
115 120 125

Asp Ala Asn Gly His Tyr Asn Lys Val His Glu Asp Leu Met Leu Pro
130 135 140

Phe Asp Glu Phe Leu Ala Leu Asn Gly Cys Glu Ala Ala Arg Asp Leu
145 150 155 160

Trp Ile Asn Pro Phe Thr Ala Phe Gly Tyr His Phe Asp Asn Val
165 170 175

Pro Ala Ala Tyr Val Leu Lys Tyr Leu Asp Phe Val Thr Met Met Ser
180 185 190

Phe Ala Lys Gly Asp Leu Trp Thr Trp Ala Asp Gly Thr Gln Ala Met
195 200 205

Phe Glu His Leu Asn Ala Thr Leu Glu His Pro Ala Glu Arg Asn Val
210 215 220

Asp Ile Thr Arg Ile Thr Arg Glu Asp Gly Lys Val His Ile His Thr
225 230 235 240

Thr Asp Trp Asp Arg Glu Ser Asp Val Leu Val Leu Thr Val Pro Leu
245 250 255

Glu Lys Phe Leu Asp Tyr Ser Asp Ala Asp Asp Glu Arg Glu Tyr
260 265 270

Phe Ser Lys Ile Ile His Gln Gln Tyr Met Val Asp Ala Cys Leu Val
 275 280 285
 Lys Glu Tyr Pro Thr Ile Ser Gly Tyr Val Pro Asp Asn Met Arg Pro
 290 295 300
 Glu Arg Leu Gly His Val Met Val Tyr Tyr His Arg Trp Ala Asp Asp
 305 310 315 320
 Pro His Gln Ile Ile Thr Thr Tyr Leu Leu Arg Asn His Pro Asp Tyr
 325 330 335
 Ala Asp Lys Thr Gln Glu Glu Cys Arg Gln Met Val Leu Asp Asp Met
 340 345 350
 Glu Thr Phe Gly His Pro Val Glu Lys Ile Ile Glu Glu Gln Thr Trp
 355 360 365
 Tyr Tyr Phe Pro His Val Ser Ser Glu Asp Tyr Lys Ala Gly Trp Tyr
 370 375 380
 Glu Lys Val Glu Gly Met Gln Gly Arg Arg Asn Thr Phe Tyr Ala Gly
 385 390 395 400
 Glu Ile Met Ser Phe Gly Asn Phe Asp Glu Val Cys His Tyr Ser Lys
 405 410 415
 Asp Leu Val Thr Arg Phe Phe Val
 420

<210> 62
 <211> 7
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> RBS
 <222> (1)..(7)

<400> 62
 aaggaag

7

<210> 63
 <211> 1073
 <212> DNA
 <213> Propionibacterium acnes

<400> 63

gccgggcggg cacgattgac gaatttccgc acactggatg gcggaaacaaa ggtgtcgta 60
 tttccctgga tcaccattgt tggtggtgcc tgaggagtga tccaggtgga actgttgaca 120
 gcgcgataac ggtcgaaaa ttgctgggg gtgccaccga tatacattt ggcggcattg 180
 cccgcgctca gtgtgggtac cgactcgacg gtaccgacat ccaccgttgg atagaggcg 240
 aggactgact tcggggcccg tattgagccg caggaactct tcaactttcc actggcgccg 300
 ccgtaggcga gattaatggc cattccacca ccagcggaat caccatgtat cgataacctgt 360
 gaagggtcgc caccgagttc tttcacgtgg gacaggctcc aggcccaggc acatgcgacc 420
 tggttttgggg cggtattcca ggtgggtgg ccctgggtgg ccagggtgta cgagggcga 480
 atgactaacc agccatgatc ggaaaaccat ctcaacgtgg cggcatggt ggcgtcggtg 540

ctccatcctt caccatgaat gtcgacaagt accggggcat tgggttatg ggcacggtag 600
atctggccg tctcgtaagg gccgatcca taccggaccg ttctcgtaagg gtggtcggac 660
atcgacgaca ccgcagctgc cgagacgacg ttgatacgtc caccggggcg gtccgtgatc 720
cacgcgtcg tcgcccgtgc cgccactggc acgatgaggg ccatcaccga gaagacaacg 780
gccaccactc gcagaccacc tcgtccaaa agagcagga cgaaggcgat gacggcgatg 840
accagagccg gtacagccaa cgatcccacc agaacggagg agatgaaggt gagggcattg 900
tgtgagggga ggatcgccgc cactgaccac gccagtaccg gcagggtcag gatcagcccg 960
acgagaccgg aagtgatgca tagccagaa tgacgggagg ttctcgatc agccacgcgt 1020
ccaccgtact cacggacat ggtcgatagg atctcgatc aggaggacc cat 1073

<210> 64

<211> 358

<212> PRT

<213> Propionibacterium acnes

<400> 64

Met Gly Pro Ser Cys Ala Lys Ile Leu Ser Thr Met Ser Arg Glu Tyr
1 5 10 15

Gly Gly Arg Val Ala Asp Thr Lys Thr Ser Arg His Ser Trp Leu Arg
20 25 30

Ile Thr Ser Gly Leu Val Gly Leu Ile Leu Thr Leu Pro Val Leu Ala
35 40 45

Trp Ser Val Ala Ala Ile Leu Pro Ser His Asn Ala Leu Thr Phe Ile
50 55 60

Ser Ser Val Leu Val Gly Ser Leu Ala Val Pro Ala Leu Val Ile Ala
65 70 75 80

Val Ile Ala Phe Val Leu Ala Leu Leu Gly Arg Gly Gly Leu Arg Val
85 90 95

Val Ala Val Val Phe Ser Val Met Ala Leu Ile Val Pro Val Ala Ala
100 105 110

Thr Ala Thr Thr Ala Trp Ile Thr Asp Arg Pro Gly Gly Arg Ile Asn
115 120 125

Val Val Ser Ala Ala Ala Val Ser Ser Met Ser Asp His Pro Asp Glu
130 135 140

Thr Val Arg Tyr Gly Ser Gly Pro Asp Glu Thr Ala Gln Ile Tyr Arg
145 150 155 160

Ala His Asn His Asn Ala Pro Val Leu Val Asp Ile His Gly Glu Gly
165 170 175

Trp Ser Thr Asp Ala Thr Met Pro Ala Thr Leu Arg Trp Phe Ser Asp
180 185 190

His Gly Trp Leu Val Ile Arg Pro Ser Tyr Thr Leu Ala Thr Gln Gly
195 200 205

His Pro Thr Trp Asn Thr Ala Pro Lys Gln Val Ala Cys Ala Trp Ala
210 215 220

Trp Ser Leu Ser His Val Lys Glu Leu Gly Gly Asp Pro Ser Gln Val
225 230 235 240

Ser Ile Met Gly Asp Ser Ala Gly Gly Gly Met Ala Ile Asn Leu Ala
 245 250 255
 Tyr Gly Ala Ala Ser Gly Lys Leu Lys Ser Ser Cys Gly Ser Ile Arg
 260 265 270
 Ala Pro Lys Ser Val Leu Ala Leu Tyr Pro Thr Val Asp Val Gly Thr
 275 280 285
 Val Glu Ser Val Thr Thr Leu Ser Ala Gly Asn Ala Ala Lys Met Tyr
 290 295 300
 Ile Gly Gly Thr Pro Lys Gln Phe Pro Asp Arg Tyr Arg Ala Val Asn
 305 310 315 320
 Ser Ser Thr Trp Ile Thr Pro Gln Ala Pro Pro Thr Met Val Ile Gln
 325 330 335
 Gly Asn His Asp Thr Phe Val Pro Pro Ser Ser Val Arg Lys Phe Val
 340 345 350
 Asn Arg Ala Arg Pro Ala
 355

<210> 65

<211> 783

<212> DNA

<213> Propionibacterium acnes

<220>

<221> CDS

<222> (1)..(783)

<400> 65

atg tcc ata aca cca cga aag tgc aag gct gcc gcc ctt gcc aca gcg	48
Met Ser Ile Thr Pro Arg Lys Cys Lys Ala Ala Ala Leu Ala Thr Ala	
1 5 10 15	

ccg gtg gcc gct gcc ctc ggt gct tac gga ttt ctt aaa ggg gcg acg	96
Pro Val Ala Ala Ala Leu Gly Ala Tyr Gly Phe Leu Lys Gly Ala Thr	
20 25 30	

aag ttc tat tcc agc cag gtt aac gga act ccc gag cag tac aag atg	144
Lys Phe Tyr Ser Ser Gln Val Asn Gly Thr Pro Glu Gln Tyr Lys Met	
35 40 45	

acc ctt cct ggt gac gac ctc gtc ccg gaa ggt tcg ccg cgc ttc aag	192
Thr Leu Pro Gly Asp Asp Leu Val Pro Glu Gly Ser Pro Arg Phe Lys	
50 55 60	

cgc ctc acc cat gtg gag gat ctc gac gcc ccc tgc gac gag gtc tgg	240
Arg Leu Thr His Val Glu Asp Leu Asp Ala Pro Cys Asp Glu Val Trp	
65 70 75 80	

aag cac gtc tac cag ctc aac acc acg acc gcc ggc ttc tac tcc ttc	288
Lys His Val Tyr Gln Leu Asn Thr Thr Ala Gly Phe Tyr Ser Phe	
85 90 95	

acc ttc ttc gag aag atg ttc gga ctg tcg gtc gac aac acc ttc atg	336
-----------------------------------------------------------------	-----

Thr Phe Phe Glu Lys Met Phe Gly Leu Ser Val Asp Asn Thr Phe Met			
100	105	110	
gtg gaa cag gct tgg cag gcc ccg gac tac tac aag ccc ggt gac atg	384		
Val Glu Gln Ala Trp Gln Ala Pro Asp Tyr Tyr Lys Pro Gly Asp Met			
115	120	125	
ttc tgt tgg agt tac gcc ggt ttc ggt gcc gag gtc gcc gac atg gtc	432		
Phe Cys Trp Ser Tyr Ala Gly Phe Gly Ala Glu Val Ala Asp Met Val			
130	135	140	
ccc ggc aag tat ctg gtg tgg ttc gct gac acc cgt gac ggc acc agg	480		
Pro Gly Lys Tyr Leu Val Trp Phe Ala Asp Thr Arg Asp Gly Thr Arg			
145	150	155	160
aca ccg ggc gca agt ttc ctg cta ccg cct gga atg ccg tgg aac ccg	528		
Thr Pro Gly Ala Ser Phe Leu Leu Pro Pro Gly Met Pro Trp Asn Arg			
165	170	175	
tgg agt tgg gtc atc gcc ctg gaa ccc ctc gac agt ggc aac ccg acg	576		
Trp Ser Trp Val Ile Ala Leu Glu Pro Leu Asp Ser Gly Asn Arg Thr			
180	185	190	
cgc atc tac tcc ccg tgg aac atc tcg gcc tcc gag gag tcc agt ccg	624		
Arg Ile Tyr Ser Arg Trp Asn Ile Ser Ala Ser Glu Glu Ser Ser Pro			
195	200	205	
atc tcg gtc ttc ctc atg gat ctg gtc atg atg gac ggc ggc ggc atg	672		
Ile Ser Val Phe Leu Met Asp Leu Val Met Met Asp Gly Gly Gly Met			
210	215	220	
gtg aac cgt ccg atg ttc caa ggg ctg gag aag gct gcc gtc gga act	720		
Val Asn Arg Arg Met Phe Gln Gly Leu Glu Lys Ala Ala Val Gly Thr			
225	230	235	240
gct cgc aag aac atc gtt cct gcg cgc cta tca gcg gtt cat ggg caa	768		
Ala Arg Lys Asn Ile Val Pro Ala Arg Leu Ser Ala Val His Gly Gln			
245	250	255	
gtc eta ccg cac tga	783		
Val Leu Arg His			
260			

<210> 66

<211> 260

<212> PRT

<213> Propionibacterium acnes

<400> 66

Met Ser Ile Thr Pro Arg Lys Cys Lys Ala Ala Ala Leu Ala Thr Ala
 1 5 10 15

Pro Val Ala Ala Ala Leu Gly Ala Tyr Gly Phe Leu Lys Gly Ala Thr
 20 25 30

Lys Phe Tyr Ser Ser Gln Val Asn Gly Thr Pro Glu Gln Tyr Lys Met
 35 40 45

Thr Leu Pro Gly Asp Asp Leu Val Pro Glu Gly Ser Pro Arg Phe Lys
 50 55 60

Arg Leu Thr His Val Glu Asp Leu Asp Ala Pro Cys Asp Glu Val Trp
 65 70 75 80

Lys His Val Tyr Gln Leu Asn Thr Thr Ala Gly Phe Tyr Ser Phe

85	90	95
Thr Phe Phe Glu Lys Met Phe Gly Leu Ser Val Asp Asn Thr Phe Met		
100	105	110
Val Glu Gln Ala Trp Gln Ala Pro Asp Tyr Tyr Lys Pro Gly Asp Met		
115	120	125
Phe Cys Trp Ser Tyr Ala Gly Phe Gly Ala Glu Val Ala Asp Met Val		
130	135	140
Pro Gly Lys Tyr Leu Val Trp Phe Ala Asp Thr Arg Asp Gly Thr Arg		
145	150	155
Thr Pro Gly Ala Ser Phe Leu Leu Pro Pro Gly Met Pro Trp Asn Arg		
165	170	175
Trp Ser Trp Val Ile Ala Leu Glu Pro Leu Asp Ser Gly Asn Arg Thr		
180	185	190
Arg Ile Tyr Ser Arg Trp Asn Ile Ser Ala Ser Glu Glu Ser Ser Pro		
195	200	205
Ile Ser Val Phe Leu Met Asp Leu Val Met Met Asp Gly Gly Gly Met		
210	215	220
Val Asn Arg Arg Met Phe Gln Gly Leu Glu Lys Ala Ala Val Gly Thr		
225	230	235
Ala Arg Lys Asn Ile Val Pro Ala Arg Leu Ser Ala Val His Gly Gln		
245	250	255
Val Leu Arg His		
260		

<210> 67

<211> 7

<212> DNA

<213> Propionibacterium acnes

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<220>

<221> RBS

<222> (1)..(7)

<400> 67

gaaggag

7

<210> 68

<211> 582

<212> DNA

<213> Propionibacterium acnes

<220>

<221> CDS

<222> (1)..(582)

<400> 68

atg	gat	act	tca	gtc	aat	gtc	gac	acg	tcg	tca	aga	ccg	gcg	cac	gaa		48
Met	Asp	Thr	Ser	Val	Asn	Val	Asp	Thr	Ser	Ser	Arg	Pro	Ala	His	Glu		
1				5				10				15					

ccg	gcc	acc	gct	ccc	ggt	cgt	ttc	gtc	gtc	aga	gat	gcc	tgt	cac	gag		96
Pro	Ala	Thr	Ala	Pro	Gly	Arg	Phe	Val	Val	Arg	Asp	Ala	Cys	His	Glu		
20								25				30					

gac	ctg	cct	gaa	gcc	gct	gtt	cag	gcc	gtg	tgc	gtc	cga	gag	atc		144
Asp	Leu	Pro	Glu	Ala	Ala	Val	Gln	Ala	Val	Cys	Val	Arg	Glu	Ile		
35								40				45				

ggc cag ggg gtg atc cct aat gac gtc ctt acc gag gtc act ggc ccc 192
 Gly Gln Gly Val Ile Pro Asn Asp Val Leu Thr Glu Val Thr Gly Pro
 50 55 60

 ggt atc gtc cac acc acc att gag cag tgg aac cac ttt atg gat gat 240
 Gly Ile Val His Thr Thr Ile Glu Gln Trp Asn His Phe Met Asp Asp
 65 70 75 80

 ggt gcg atc ttc aag atc ctt gtt gat cgc ctc gat atg agg act gtc 288
 Gly Ala Ile Phe Lys Ile Leu Val Asp Arg Leu Asp Met Arg Thr Val
 85 90 95

 ggg gtt gcc atg gcc cgg gtc tct aca agt tct gat gct ccc aca ccg 336
 Gly Val Ala Met Ala Arg Val Ser Thr Ser Ser Asp Ala Pro Thr Pro
 100 105 110

 tgg gag atc gcg acc ctc cat gta ctg cca gag gcg cga aac tgc gga 384
 Trp Glu Ile Ala Thr Leu His Val Leu Pro Glu Ala Arg Asn Cys Gly
 115 120 125

 gcg tca gac aac ctc ctc gat gct tgt atc ggg aac cgg tcg gcc tat 432
 Ala Ser Asp Asn Leu Leu Asp Ala Cys Ile Gly Asn Arg Ser Ala Tyr
 130 135 140

 gtg tgg gtc ttt gcc gat aat gct cgc gcc att tcg ttc tac caa cgc 480
 Val Trp Val Phe Ala Asp Asn Ala Arg Ala Ile Ser Phe Tyr Gln Arg
 145 150 155 160

 cat ggg ttc cac gtc gac gcg gcc gac ggt gcc gtt gac gat tcc ctc 528
 His Gly Phe His Val Asp Ala Ala Asp Gly Ala Val Asp Asp Ser Leu
 165 170 175

 ggc ggg gta gag ctg cag cgg ctg atc cgc gag gac atc atc gag tcg 576
 Gly Gly Val Glu Leu Gln Arg Leu Ile Arg Glu Asp Ile Ile Glu Ser
 180 185 190

 cag tga 582
 Gln

 <210> 69
 <211> 193
 <212> PRT
 <213> Propionibacterium acnes

 <400> 69
 Met Asp Thr Ser Val Asn Val Asp Thr Ser Ser Arg Pro Ala His Glu
 1 5 10 15
 Pro Ala Thr Ala Pro Gly Arg Phe Val Val Arg Asp Ala Cys His Glu
 20 25 30
 Asp Leu Pro Glu Ala Ala Ala Val Gln Ala Val Cys Val Arg Glu Ile
 35 40 45
 Gly Gln Gly Val Ile Pro Asn Asp Val Leu Thr Glu Val Thr Gly Pro
 50 55 60
 Gly Ile Val His Thr Thr Ile Glu Gln Trp Asn His Phe Met Asp Asp
 65 70 75 80
 Gly Ala Ile Phe Lys Ile Leu Val Asp Arg Leu Asp Met Arg Thr Val
 85 90 95
 Gly Val Ala Met Ala Arg Val Ser Thr Ser Ser Asp Ala Pro Thr Pro
 100 105 110
 Trp Glu Ile Ala Thr Leu His Val Leu Pro Glu Ala Arg Asn Cys Gly

115 120 125
Ala Ser Asp Asn Leu Leu Asp Ala Cys Ile Gly Asn Arg Ser Ala Tyr
130 135 140
Val Trp Val Phe Ala Asp Asn Ala Arg Ala Ile Ser Phe Tyr Gln Arg
145 150 155 160
His Gly Phe His Val Asp Ala Ala Asp Gly Ala Val Asp Asp Ser Leu
165 170 175
Gly Gly Val Glu Leu Gln Arg Leu Ile Arg Glu Asp Ile Ile Glu Ser
180 185 190
Gln

<210> 70
<211> 7
<212> DNA
<213> Propionibacterium acnes

<220>
<221> RBS
<222> (1)..(7)

<400> 70
ggtagga

7

<210> 71
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 71
cagacatatg tccatctcgaa aggattc

27

<210> 72
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 72
ctatctcgag tcacacgaa aaccgcgtc

29

<210> 73
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus

<220>
<221> UNSURE
<222> (1)..(53)

<223> Xaa = any amino acid

<400> 73

Gly Xaa Gly Xaa Xaa Gly Xaa Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa
20 25 30

Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Gly
50

<210> 74

<211> 43

<212> PRT

<213> Homo sapiens

<400> 74

Ser Glu Ala Tyr Ser Ala Lys Ile Ala Leu Phe Gly Ala Gly Pro Ala
1 5 10 15

Ser Ile Ser Cys Ala Ser Phe Leu Ala Arg Leu Gly Tyr Ser Asp Ile
20 25 30

Thr Ile Phe Glu Lys Gln Glu Tyr Val Gly Gly
35 40

<210> 75

<211> 41

<212> PRT

<213> Agrobacterium vitis

<400> 75

Lys Val Ala Ile Val Gly Ala Gly Leu Ser Gly Leu Val Val Ala Ser
1 5 10 15

Glu Leu Leu His Ala Gly Ile Asp Asp Val Thr Leu Tyr Glu Ala Ser
20 25 30

Asp Arg Ile Gly Gly Lys Leu Trp Ser
35 40

<210> 76

<211> 45

<212> PRT

<213> Deinococcus radiodurans

<400> 76

Val Lys Thr Gly Lys Lys Val Ala Val Val Gly Ser Gly Pro Ala Gly
1 5 10 15

Leu Ala Ala Ala Gln Gln Leu Ala Arg Ala Gly His Asp Val Thr Val
20 25 30

Phe Glu Lys Asn Asp Arg Val Gly Gly Arg Ile Glu Gln

35

40

45

<210> 77

<211> 37

<212> PRT

<213> Arthrobacter nicotinovorans

<400> 77

Val Val Gly Gly Gly Phe Ser Gly Leu Lys Ala Ala Arg Asp Leu Thr
1 5 10 15

Asn Ala Gly Lys Lys Val Leu Leu Glu Gly Gly Glu Arg Leu Gly
20 25 30

Gly Arg Ala Tyr Ser
35

<210> 78

<211> 52

<212> PRT

<213> Synechocystis sp.

<400> 78

Arg Ile Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ala Thr Ala Val
1 5 10 15

Glu Leu Val Asp Ala Gly His Glu Val Glu Leu Tyr Glu Ala Arg Ser
20 25 30

Phe Ile Gly Gly Lys Val Gly Ser Trp Val Asp Gly Asp Gly Asn His
35 40 45

Ile Glu Met Gly
50

<210> 79

<211> 57

<212> PRT

<213> Cercospora nicotianae

<400> 79

Ser Thr Ser Lys Arg Pro Thr Ala Ile Val Ile Gly Ser Gly Val Gly
1 5 10 15

Gly Val Ser Thr Ala Ala Arg Leu Ala Arg Ala Gly Phe His Val Thr
20 25 30

Val Leu Glu Lys Asn Asn Phe Thr Gly Gly Arg Cys Ser Leu Ile His
35 40 45

His Glu Gly Tyr Arg Phe Asp Gln Gly
50 55

<210> 80

<211> 52

<212> PRT

<213> Zea mays

<400> 80
Arg Val Ile Val Val Gly Ala Gly Met Ser Gly Ile Ser Ala Ala Lys
1 5 10 15
Arg Leu Ser Glu Ala Gly Ile Thr Asp Leu Leu Ile Leu Glu Ala Thr
20 25 30
Asp His Ile Gly Gly Arg Met His Lys Thr Asn Phe Ala Gly Ile Asn
35 40 45
Val Glu Leu Gly
50

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